

## SEQUENCE LISTING

5

## (1) GENERAL INFORMATION:

10 (i) APPLICANT:  
(A) NAME: Boehringer Ingelheim International GmbH  
(B) STREET: Binger Strasse 173  
(C) CITY: Ingelheim am Rhein  
(E) COUNTRY: Germany  
15 (F) POSTAL CODE (ZIP): 55216  
(G) TELEPHONE: 06132/772282  
(H) TELEFAX: 06132/774377

20 (ii) TITLE OF INVENTION: Tumor-associated Antigen

(iii) NUMBER OF SEQUENCES: 28

25 (iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

35 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 679 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
45 (ii) MOLECULE TYPE: cDNA to mRNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO  
50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: homo sapiens  
(F) TISSUE TYPE: Melanoma  
55 (ix) FEATURE:  
(A) NAME/KEY: 3'UTR

(B) LOCATION:340..679

- 5 (ix) FEATURE:  
 (A) NAME/KEY: 5'UTR  
 (B) LOCATION:1..9
- 10 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION:10..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

15	CGACGGGGCG ATG CTG ATG GGC CAG GAG GGC CTG GCA TTC CTG ATG GCC Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala 1 5 10	48
20	CAG GGG GCA ATG CTG GCG GGC CAG GAG AGG CGG GTG CCA CGG GCG GCA Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala 15 20 25	96
25	GAG GTC CCC CGG CGG CAG CGG CAG CAA CGG CCT CGG CGC CGA GAG GAG Glu Val Pro Gly Ala Gln Gly Gln Gly Pro Arg Gly Arg Glu Glu 30 35 40 45	144
30	GCG CCC CGG GTC CGC ATG CGG GTG CGG CCT CTG CGC AGG ATG GAA Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu 50 55 60	192
35	GGT GCC CCT CGG GGG CCA GGA CGG ACA GCA GCC GGC TGC TTC AGT TGC Gly Ala Pro Ala Gly Pro Gly Arg Thr Ala Ala Cys Phe Ser Cys 65 70 75	240
40	ACA TCA CGA TGC CCT TCT CGT CGC CCA TGG AAG CGG AGC TGG TCC GCA Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala 80 85 90	288
45	GGA TCC TGT CGC GGG ATG CGG CAC CCT TCC CGC GAC CAG GGG CGG TTC Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe 95 100 105	336
50	TGA AGGACTTCAC CGTGTCGGC AAATCTACTGT TTATCGACT GACTGCTCCA * 110	389
55	GAACAAAGGC AACTGCAGCT CTCATCAGC TCTGCTCTOC ACCAGCTTTTC CCTGTTGATC TGATCAOGC AGTGCTTTCT GCGCGTGTIT TTGGCTCAGG CTCCTCAGG GCAGAGGCGC TAAGCCAGC CTGGCGCGGC TTCTAGGTC ATGCTCTC CCTAGGGAA TGGTOOCAGC AOGAGTGGGC AGTTCAATTGT GGGGCGCTGA TTGTGTTGTOG CTGGAGGAGG ACGGCTTACA TGTTTGTTC TGTAGAAAAAT AAAGCTGAGC TAAGAAAAAA AAAAAAAAAA	449 509 569 629 679

## (2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
15 1 5 10 15

Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
20 25 30

20 Gly Ala Gln Gly Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro  
50 55 60

25 Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg  
65 70 75 80

30 Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys  
85 90 95

Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe \*

100 105 110

35

## (2) INFORMATION FOR SEQ ID NO: 3:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 767 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: homo sapiens  
(F) TISSUE TYPE: Melanoma

55 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 54..596

## (ix) FEATURE:

- (A) NAME/KEY: 3'UTR  
(B) LOCATION:597..767

5

## (ix) FEATURE:

- (A) NAME/KEY: 5'UTR  
(B) LOCATION:1..53

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCCTGTTGG GCGCTGACCT TCTCTCTGAG AGCGGGCAG AGGCCTCGGA GCC ATG	56
Met	1
CAG GOC GAA GGC CAG GGC ACA GGG GGT TCG ACG GGC GAT GCT GAT GGC	104
Gln Ala Glu Gly Gln Gly Thr Gly Ser Thr Gly Asp Ala Asp Gly	
5 10 15	
CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	152
Pro Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
20 25 30	
CCA GGA GAG GCG GGT GGC ACG GGC AGA GGT CCG CCG GGC GCA CGG	200
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
35 40 45	
GCA GCA AGG GGC TCG GGG CGG AGA GGA GGC GGC CGG CGG GGT CGG CAT	248
Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
50 55 60 65	
GGC GGT GGC CCT TCT CGG CAG GAT GGA AGG TGC CCG TGC GGG GGC AGG	296
Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	
70 75 80	
AGG CGG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TCG	344
Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	
85 90 95	
TGG CGC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG GAT GGC	392
Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	
100 105 110	
GCA CCT CTC CCC CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TCC	440
Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	
115 120 125	
GGC AAC CTA CTG TTT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG	488
Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	
130 135 140 145	
CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG	536
Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	
150 155 160	

	AAT ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly 165                   170                   175	584
5	CAG AGG CGC TAA GGGAGGCTTG GGGGGGCTTC CTAGGTCTATG OCTOCTCCCC Gln Arg Arg * 180	636
10	TACGGAAATGG TCCAGGCAOG AGTGGCCAGT TCATTGTTGGG GCGCTGATTG TTTGTOGCTG GAGGAGGAOG CCTTACATGT TTGTTCTGT AGAAAAATAAA CCTGAGCTAC GAAAAAAAAA AAAAAAA A	696
15		756
		767

## (2) INFORMATION FOR SEQ ID NO: 4:

20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 180 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
30	Met Gln Ala Glu Gly Gln Gly Thr Gly Ser Thr Gly Asp Ala Asp 1               5                   10                   15
	Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly 20              25                   30
35	Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala 35              40                   45
40	Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro 50              55                   60
	His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala 65              70              75                   80
45	Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe 85              90                   95
	Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp 100            105                   110
50	Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val 115            120                   125
55	Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln 130            135                   140
	Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met 145            150                   155                   160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser  
 165 170 175  
 Gly Gln Arg Arg \*  
 180  
 5

(2) INFORMATION FOR SEQ ID NO: 5:

- 15                     (i) SEQUENCE CHARACTERISTICS:  
                           (A) LENGTH: 993 base pairs  
                           (B) TYPE: nucleic acid  
                           (C) STRANDEDNESS: single  
                           (D) TOPOLOGY: linear

20                     (ii) MOLECULE TYPE: cDNA to mRNA  
  
                           (iii) HYPOTHETICAL: NO  
  
                           (iv) ANTI-SENSE: NO  
  
                           (vi) ORIGINAL SOURCE:  
                               (A) ORGANISM: homo sapiens  
                               (F) TISSUE TYPE: Melanoma  
  
25                     (ix) FEATURE:  
                               (A) NAME/KEY: 5'UTR  
                               (B) LOCATION:1..55  
  
30                     (ix) FEATURE:  
                               (A) NAME/KEY: CDS  
                               (B) LOCATION:56..688  
  
35                     (ix) FEATURE:  
                               (A) NAME/KEY: 3'UTR  
                               (B) LOCATION:689..993

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

	GCAATCCCTGTCGGGCGCTGACCTTCTCTCTGAGAGCGGGCAGAGGCTCGAGAGCTGAGAGCTGATG	58
45		Met 1
	CAG GGC GAA GGC CAG GGC ACA CGG GGT TCG ACG GGC GAT CCT GAT GCC	106
	Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
50	CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA CGG GGC AAT CCT GGC GGC	154
	Pro Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
55	CCA GGA GAG CGG GGT GGC ACG GGC GGC AGA GGT CCC CGG GGC GCA CGG	202
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
	35 40 45	
	GCA GCA AGG GGC TCG CGG CGG AGA GGA GGC GGC CGG CGG CGT CGG CAT	250

	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
5	GGC GGT GGC GCT TCT GCG CAG GAT GGA AGG TGC ACC TGC GGG GGC AGG Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	298
	70 75 80	
10	AGG COG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TCG Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	346
	85 90 95	
15	TGG CCC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG GAT GGC Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	394
	100 105 110	
	GCA CCT CTC CCC CGA CCA GGG CGG GTT CTG AAG GAC TTC ACC GTG TCC Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	442
	115 120 125	
20	GGC AAC CTA CTG TTT ATG TCA GTT CGG GAC CAG GAC AGG GAA GGC GCT Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala	490
	130 135 140 145	
25	GGG CGG ATG AGG GTG GTG GGT TGG CGG CTG GGA TCC GGC TCC CGG GAG Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro Glu	538*
	150 155 160	
30	GGG CAG AAA GCT AGA GAT CTC AGA ACA CCC AAA CAC AAG GTC TCA GAA Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu	586
	165 170 175	
35	CAG AGA CCT GGT ACA CCA GGC CGG CGG CCA CCC GAG GGA GGC CAG GGA Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Glu Gly Ala Gln Gly	634
	180 185 190	
	GAT GGG TGC AGA GGT GTC GCC TTT AAT GTG ATG TIC TCT GGC CCT CAC Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His	682
	195 200 205	
40	ATT TAG CGCAGCTGACT GCTGCCAGACC ACCGCCAACT GCAGCTCTCC ATCAGCTCT Ile *	738
	210	
45	GCTCCAGCA GCTTTOOCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCGCC GTGTTTTTGG CTCAGGGCTCC CTCAGGGCAG AGGGGCTAAG CCCAGCTGG CGGCGCTCC TAGGTCATGC	798
	CTCCCTCCCT AGGGAAATGGT CCAGCAOGA GTGGCAGIT CATTGTGGGG GCGTGAATTGT	858
50	TTGTCGCTGG AGGAGGAOGG CTTACATGTT TGTTCTGTA GAAAATAAAG CTGAGCTAOG AAAAAAAAAAAA AAAAAA	918
		993

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(2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

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## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10 Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp  
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly  
20 25 30

15 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala  
35 40 45

20 Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro  
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala  
65 70 75 80

25 Arg Arg Pro Asp Ser Arg Leu Leu Gln Ile His Ile Thr Met Pro Phe  
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp  
100 105 110

30 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val  
115 120 125

35 Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly  
130 135 140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro  
145 150 155 160

40 Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser  
165 170 175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Glu Gly Ala Gln  
180 185 190

45 Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro  
195 200 205

50 His Ile \*  
210

55

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 752 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

15

(ix) FEATURE:

(A) NAME/KEY: 5'UTR  
 (B) LOCATION: 1..53

20

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 54..596

25

(ix) FEATURE:

(A) NAME/KEY: 3'UTR  
 (B) LOCATION: 597..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

30	ATCTCTGGG GCGCTGACCT TCTCTCTGAG AGCCGGGCAG AGCTCTGGGA GCG ATG	56
	Met	
	1	
35	CAG GCG GAA GGC CGG GGC ACA GGG GGT TCG ACG GCG GAT GCT GAT GGC	104
	Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
40	CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG CCC AAT GCT GGC GGC	152
	Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
45	CCA GGA GAG CGG GGT GCG ACG GGC CGC AGA GGT CCC CGG GGC CCA GGG	200
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
	35 40 45	
50	GCA GCA AGG GCG TCG CGG CGG GGA CGA CGC GOC CGG CGG GGT CGT CAT	248
	Ala Ala Arg Ala Ser Gly Pro Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
55	GCC GGC CGG GCT TCA GGG CTG AAT GGA TGC TGC AGA TGC GGG GCG AGG	296
	Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg	
	70 75 80	
60	GGG CGG GAG AGC CGC CTG CTT GAG TTC TAC CTC GGC ATG CCT TTC CGG	344
	Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala	
	85 90 95	
65	ACA CGC ATG GAA GCA GAG CTG GCG CGC AGG AGC CTG GCG CAG GAT GCG	392

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	Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala			
	100	105	110	
5	CCA CGG CTT CCC GIG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TCC Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser		440	
	115	120	125	
10	GCG AAC ATA CTG ACT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu		488	
	130	135	140	145
15	CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp		536	
	150	155	160	
20	ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly		584	
	165	170	175	
25	CAG AGG CGC TAA GCCCCGCTTG GGGCGCGCTTC CTAGGTCTATG CCTCCCTCCCC Gln Arg Arg *		636	
	180			
	TAGGGAATGG TOCCAGGAOG AGTGGCCAGT TCATITGIGGG GCGCTGATTG TTITGTCGCTG		696	
	GAGGGAGGAGC GCCTTACATGT TTGTTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAAA		752	

30 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Gln	Ala	Glu	Gly	Arg	Gly	Thr	Gly	Ser	Thr	Gly	Asp	Ala	Asp
1							5						10	15

45	Gly	Pro	Gly	Pro	Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly
	20					25							30		

50	Gly	Pro	Gly	Glu	Ala	Gly	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala
				35				40			45					

55	Gly	Ala	Ala	Arg	Ala	Ser	Gly	Pro	Gly	Gly	Ala	Pro	Arg	Gly	Pro	
	50					55					60					

65	His	Gly	Gly	Ala	Ala	Ser	Gly	Leu	Asn	Gly	Cys	Cys	Arg	Cys	Gly	Ala
						70			75				80			

85	Arg	Gly	Pro	Glu	Ser	Arg	Leu	Leu	Glu	Phe	Tyr	Leu	Ala	Met	Pro	Phe
							90						95			

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Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp  
 100 105 110

5 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val  
 115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln  
 130 135 140

10 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met  
 145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser  
 15 165 170 175

Gly Gln Arg Arg \*  
 180

20

## (2) INFORMATION FOR SEQ ID NO: 9:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- 35 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: homo sapiens
- 40 (ix) FEATURE:
- (A) NAME/KEY: 5'UTR
  - (B) LOCATION: 1..93
- 45 (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 94..270
- 50 (ix) FEATURE:
- (A) NAME/KEY: 3'UTR
  - (B) LOCATION: 271..752
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
- 55 ATCTCTGTGG GCGCTGACT TCTCTCTGAG AGCCGGCCAG AGGCTCGGGA GCGATCCAGG 60  
 CGGAAGGCG GGGCACAGGG GGTTOGACGG GCG ATG CTG ATG GCC CAG GAG GCC 114  
 Met Leu Met Ala Gln Glu Ala

(2) INFORMATION FOR SEQ ID NO: 10:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
1 5 10 15

5 Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
20 25 30

10 Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45

Gly Val Arg Met Ala Ala Arg Leu Gln Gly \*  
50 55

15

## 2) INFORMATION FOR SEQ ID NO: 11:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

30 Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
1 5 10....

## 35 2) INFORMATION FOR SEQ ID NO: 12:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
1 5 10.

50

## (2) INFORMATION FOR SEQ ID NO: 13:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

5 GGTGACACTA TAGAAGGTAC G

21

10 (2) INFORMATION FOR SEQ ID NO: 14:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

20 TGATGTGCAA CTGAAGCAGG..... 20

25 (2) INFORMATION FOR SEQ ID NO: 15:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

35 GCACTCGCTG ATCCACATCA A 21

40 (2) INFORMATION FOR SEQ ID NO: 16:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

50 CGACTCACTA TAGGGAGAGA G 21

## (2) INFORMATION FOR SEQ ID NO: 17:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: synthetic DNA

GCACATCAAG ATGOCITTCCT CGTOG

25

15

## (2) INFORMATION FOR SEQ ID NO: 18:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: synthetic DNA

CACACAAAAGC TTGGCTTACG GGCCTCTGOC TG.....32

30

## (2) INFORMATION FOR SEQ ID NO: 19:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: synthetic DNA

CACACAGGAT CCATGGATGC TGCAGATGOG.....30

45

## (2) INFORMATION FOR SEQ ID NO: 20:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: synthetic DNA

GAAGAACATA TGCTGATGCC CCAGGAGGC

29

## (2) INFORMATION FOR SEQ ID NO: 21:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: synthetic DNA

TTAAAGATCT CAGAACCGCC CCTGGTGC

28

15

## (2) INFORMATION FOR SEQ ID NO: 22:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: synthetic DNA

ttactcgaga tgctgatggc ccagg.....25

30

## (2) INFORMATION FOR SEQ ID NO: 23:

- 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: synthetic DNA

aaggtaacctt gaacogccccc tggtag .....26

45

## 2) INFORMATION FOR SEQ ID NO: 24:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Phe Leu Met Ala Gln Gly Ala Met Leu  
1 5 9

5

2) INFORMATION FOR SEQ ID NO: 25:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

20

Ala Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5 10

25

2) INFORMATION FOR SEQ ID NO: 26:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5 9

40

2) INFORMATION FOR SEQ ID NO: 27:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

55

Tyr Tyr Met Asn Gly Thr Met Ser Gln Val  
1 5 10

## 2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Glu Val Asp Pro Ile Gly His Leu Tyr  
1               5               9

15